

#6
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TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana

<120> 58860, A HUMAN CHOLESTERYL ESTER
HYDROLASE AND USES THEREFOR

<130> MPI2001-026P1RNM

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Cys	Gly	Thr	Leu	Asn	Ala	Gly	Gly	Phe	Leu	Asp	Leu	Glu	Asn	Glu	Val	
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aat	cct	gag	gtg	tgg	atg	aat	act	agt	gaa	atc	atc	atc	tac	aat	ggc	147
Asn	Pro	Glu	Val	Trp	Met	Asn	Thr	Ser	Glu	Ile	Ile	Ile	Tyr	Asn	Gly	
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tac	ccc	agt	gaa	gag	tat	gaa	gtc	acc	act	gaa	gat	ggg	tat	ata	ctc	195
Tyr	Pro	Ser	Glu	Glu	Tyr	Glu	Val	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Leu	
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Leu	Val	Asn	Arg	Ile	Pro	Tyr	Gly	Arg	Thr	His	Ala	Arg	Ser	Thr	Gly	
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Pro	Arg	Pro	Val	Val	Tyr	Met	Gln	His	Ala	Leu	Phe	Ala	Asp	Asn	Ala	
		80					85					90				

tac	tgg	ctt	gag	aat	tat	gct	aat	gga	agc	ctt	gga	ttc	ctt	cta	gca	339
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Tyr	Trp	Leu	Glu	Asn	Tyr	Ala	Asn	Gly	Ser	Leu	Gly	Phe	Leu	Leu	Ala		
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gat	gca	ggt	tat	gat	gta	tgg	atg	gga	aac	agt	cgg	gga	aac	act	tgg	387	
Asp	Ala	Gly	Tyr	Asp	Val	Trp	Met	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp		
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tca	aga	aga	cac	aaa	aca	ctc	tca	gag	aca	gat	gag	aaa	ttc	tgg	gcc	435	
Ser	Arg	Arg	His	Lys	Thr	Leu	Ser	Glu	Thr	Asp	Glu	Lys	Phe	Trp	Ala		
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Phe	Ser	Phe	Asp	Glu	Met	Ala	Lys	Tyr	Asp	Leu	Pro	Gly	Val	Ile	Asp		
				145					150					155			
ttc	att	gta	aat	aaa	act	ggt	cag	gag	aaa	ttg	tat	ttc	att	gga	cat	531	
Phe	Ile	Val	Asn	Lys	Thr	Gly	Gln	Glu	Lys	Leu	Tyr	Phe	Ile	Gly	His		
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Ser	Leu	Gly	Thr	Thr	Ile	Gly	Phe	Val	Ala	Phe	Ser	Thr	Met	Pro	Glu		
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ctg	gca	caa	aga	atc	aaa	atg	aat	ttt	gcc	ttg	ggt	cct	acg	atc	tca	627	
Leu	Ala	Gln	Arg	Ile	Lys	Met	Asn	Phe	Ala	Leu	Gly	Pro	Thr	Ile	Ser		
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ttc	aaa	tat	ccc	acg	ggc	att	ttt	acc	agg	ttt	ttt	cta	ctt	cca	aat	675	
Phe	Lys	Tyr	Pro	Thr	Gly	Ile	Phe	Thr	Arg	Phe	Phe	Leu	Leu	Pro	Asn		
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Ser	Ile	Ile	Lys	Ala	Val	Phe	Gly	Thr	Lys	Gly	Phe	Phe	Leu	Glu	Asp		
				225				230						235			
aag	aaa	acg	aag	ata	gct	tct	acc	aaa	atc	tgc	aac	aat	aag	ata	ctc	771	
Lys	Lys	Thr	Lys	Ile	Ala	Ser	Thr	Lys	Ile	Cys	Asn	Asn	Lys	Ile	Leu		
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Lys	Asn	Met	Asn	Gln	Ser	Arg	Met	Asp	Val	Tyr	Met	Ser	His	Ala	Pro		
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act	ggt	tca	tca	gta	cac	aac	att	ctg	cat	ata	aaa	cag	ctt	tac	cac	915	
Thr	Gly	Ser	Ser	Val	His	Asn	Ile	Leu	His	Ile	Lys	Gln	Leu	Tyr	His		
	285				290					295					300		
tct	gat	gaa	ttc	aga	gct	tat	gac	tgg	gga	aat	gac	gct	gat	aat	atg	963	
Ser	Asp	Glu	Phe	Arg	Ala	Tyr	Asp	Trp	Gly	Asn	Asp	Ala	Asp	Asn	Met		
				305				310						315			
aaa	cat	tac	aat	cag	agt	cat	ccc	cct	ata	tat	gac	ctg	act	gcc	atg	1011	
Lys	His	Tyr	Asn	Gln	Ser	His	Pro	Pro	Ile	Tyr	Asp	Leu	Thr	Ala	Met		

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aaa gtg cct act gct att tgg gct ggt gga cat gat gtc ctc gta aca			1059
Lys Val Pro Thr Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr			
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ccc cag gat gtg gcc agg ata ctc cct caa atc aag agt ctt cat tac			1107
Pro Gln Asp Val Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr			
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ttt aag cta ttg cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc			1155
Phe Lys Leu Leu Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu			
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gat gcc cct caa cgg atg tac agt gaa atc ata gct tta atg aag gca			1203
Asp Ala Pro Gln Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala			
385	390	395	
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Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu			
35 40 45			
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg			
50 55 60			
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val			
65 70 75 80			
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu			
85 90 95			
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr			
100 105 110			
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His			
115 120 125			
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp			
130 135 140			
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn			
145 150 155 160			
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr			
165 170 175			
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg			
180 185 190			
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro			
195 200 205			
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys			

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Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys		
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Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys		240
	245	250
Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys Lys Asn Met Asn		255
	260	265
Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro Thr Gly Ser Ser		270
	275	280
Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe		285
	290	295
Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn		300
305	310	315
Gln Ser His Pro Pro Ile Tyr Asp Leu Thr Ala Met Lys Val Pro Thr		320
	325	330
Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val		335
	340	345
Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu		350
	355	360
Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln		365
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Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser		380
385	390	395

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aat gct ggt gga ttc ctt gat ttg gaa aat gaa gtg aat cct gag gtg	96
Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val	
20 25 30	
tgg atg aat act agt gaa atc atc atc tac aat ggc tac ccc agt gaa	144
Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu	
35 40 45	
gag tat gaa gtc acc act gaa gat ggg tat ata ctc ctt gtc aac aga	192
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg	
50 55 60	
att cct tat ggg cga aca cat gct agg agc aca ggt ccc cgg cca gtt	240
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val	
65 70 75 80	
gtg tat atg cag cat gcc ctg ttt gca gac aat gcc tac tgg ctt gag	288
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu	
85 90 95	

aat tat gct aat gga agc ctt gga ttc ctt cta gca gat gca ggt tat	336
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr	
100 105 110	
gat gta tgg atg gga aac agt cgg gga aac act tgg tca aga aga cac	384
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His	
115 120 125	
aaa aca ctc tca gag aca gat gag aaa ttc tgg gcc ttt agt ttt gat	432
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp	
130 135 140	
gaa atg gcc aaa tat gat ctc cca gga gta ata gac ttc att gta aat	480
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn	
145 150 155 160	
aaa act ggt cag gag aaa ttg tat ttc att gga cat tca ctt ggc act	528
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr	
165 170 175	
aca ata ggg ttt gta gcc ttt tcc acc atg cct gaa ctg gca caa aga	576
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg	
180 185 190	
atc aaa atg aat ttt gcc ttg ggt cct acg atc tca ttc aaa tat ccc	624
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro	
195 200 205	
acg ggc att ttt acc agg ttt ttt cta ctt cca aat tcc ata atc aag	672
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys	
210 215 220	
gct gtt ttt ggt acc aaa ggt ttc ttt tta gaa gat aag aaa acg aag	720
Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys	
225 230 235 240	
ata gct tct acc aaa atc tgc aac aat aag ata ctc tgg ttg ata tgt	768
Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys	
245 250 255	
agc gaa ttt atg tcc tta tgg gct gga tcc aac aag aaa aat atg aat	816
Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys Lys Asn Met Asn	
260 265 270	
cag agt cga atg gat gtg tat atg tca cat gct ccc act ggt tca tca	864
Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro Thr Gly Ser Ser	
275 280 285	
gta cac aac att ctg cat ata aaa cag ctt tac cac tct gat gaa ttc	912
Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe	
290 295 300	
aga gct tat gac tgg gga aat gac gct gat aat atg aaa cat tac aat	960
Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn	
305 310 315 320	

cag	agt	cat	ccc	cct	ata	tat	gac	ctg	act	gcc	atg	aaa	gtg	cct	act	1008
Gln	Ser	His	Pro	Pro	Ile	Tyr	Asp	Leu	Thr	Ala	Met	Lys	Val	Pro	Thr	
			325					330						335		

gct	att	tgg	gct	ggt	gga	cat	gat	gtc	ctc	gta	aca	ccc	cag	gat	gtg	1056
Ala	Ile	Trp	Ala	Gly	Gly	His	Asp	Val	Leu	Val	Thr	Pro	Gln	Asp	Val	
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gcc	agg	ata	ctc	cct	caa	atc	aag	agt	ctt	cat	tac	ttt	aag	cta	ttg	1104
Ala	Arg	Ile	Leu	Pro	Gln	Ile	Lys	Ser	Leu	His	Tyr	Phe	Lys	Leu	Leu	
		355					360					365				

cca	gat	tgg	aac	cac	ttt	gat	ttt	gtc	tgg	ggc	ctc	gat	gcc	cct	caa	1152
Pro	Asp	Trp	Asn	His	Phe	Asp	Phe	Val	Trp	Gly	Leu	Asp	Ala	Pro	Gln	
	370					375					380					

cgg	atg	tac	agt	gaa	atc	ata	gct	tta	atg	aag	gca	tat	tcc			1194
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Glu	Ala	Leu	Leu	Asp	Ala	Leu	Gly	Leu	Asp	Lys	Pro	Val	Ile	Leu	Val	
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Gly	His	Ser	Met	Gly	Gly	Ala	Leu	Ala	Ala	Ala	Tyr	Ala	Ala	Lys	Tyr	
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Pro	Glu	Glu	Arg	Val	Lys	Ala	Leu	Val	Leu	Val	Ser	Thr	Pro	Ala	Pro	
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Ala	Gly	Leu	Ser	Ser	Arg	Leu	Phe	Pro	Arg	Leu	Gly	Asn	Leu	Glu	Gly	
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Leu	Leu	Leu	Ala	Asn	Phe	Phe	Asn	Arg	Leu	Ser	Arg	Ser	Val	Glu	Ala	
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Leu	Leu	Gly	Arg	Ala	Leu	Lys	Gln	Phe	Phe	Leu	Leu	Gly	Arg	Pro	Phe	
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Arg	Pro	Gly	Glu	Thr	Asp	Gly	Gly	Asp	Gly	Leu	Leu	Gly	Tyr	Ala	Val	
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Ala	Leu	Gly	Lys	Leu	Leu	Gln	Trp	Asp	Arg	Ser	Ala	Leu	Lys	Asp	Ile	
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Lys	Val	Pro	Thr	Leu	Val	Ile	Trp	Gly	Asp	Asp	Asp	Pro	Leu	Val	Pro	
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Arg	Lys	His	Val	Lys	Leu	Asn	Pro	Ser	His	Ser	Glu	Phe	Trp	Asp	Phe
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Ser	Trp	His	Glu	Met	Gly	Met	Tyr	Asp	Leu	Pro	Ala	Met	Ile	Asp	Tyr
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Gln	Gly	Thr	Thr	Val	Phe	Phe	Val	Met	Leu	Ser	Glu	Arg	Pro	Glu	Tyr
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Asn	Glu	Lys	Ile	Lys	Ser	Phe	His	Ala	Leu	Ala	Pro	Val	Ala	Tyr	Met
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 <223> Xaa = L, I or V

<223> The amino acid at position 2 can be any amino acid

<221> VARIANT
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 <223> Xaa = L, I, V, M, S or T

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = L, I, V, M, S or T

<221> VARIANT
 <222> (6)...(6)
 <223> Xaa = H, Y, W or V

<223> The amino acid at position 8
 can be any amino acid

<221> VARIANT
 <222> (10)...(10)
 <223> Xaa = G, T, A or C

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